Claims

Claims 1-19 (Canceled)

20. (Previously presented) A method for compensating for drift in fingerprint spectra due to differences in environmental factors that affect the metabolic state of microorganisms, wherein the fingerprint spectra are selected from the group consisting of mass spectra, infrared spectra, ion-mobility spectra, gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof, comprising:

culturing under a first set of environmental factors a first microorganism and a second microorganism that is presumably metabolically similar to the first microorganism;

measuring a fingerprint spectrum of the first microorganism cultured under the first set of environmental factors and a fingerprint spectrum of the second microorganism cultured under the first set of environmental factors;

obtaining a fingerprint spectrum of the second microorganism cultured under a second set of environmental factors that differ from the first set of environmental factors and affect the metabolic state of the first and second microorganisms;

deriving a relationship between the fingerprint spectrum of the second microorganism cultured under the first set of environmental factors and the fingerprint spectrum of the second microorganism cultured under the second set of environmental factors; and,

applying the relationship derived for the second microorganism to transform the fingerprint spectrum of the first microorganism cultured under the first set of environmental factors to an expected fingerprint spectrum for the first microorganism under the second set of environmental factors that is compensated for drift due to the differences between the first and second sets of environmental factors that affect the metabolic state of the first microorganism.

21. (Previously presented) The method of claim 20, wherein culturing under a first set of environmental factors comprises culturing on a test growth medium and culturing under the second set of environmental factors comprises culturing on a library growth medium that differs from the test growth medium.

22. (Canceled)

23. (Previously presented) The method of claim 20 further including a step of identifying the first microorganism by detecting a similarity between the expected fingerprint spectrum for the second microorganism and a fingerprint spectrum of a known organism cultured under the second set of environmental factors.

24. (Previously presented) The method of claim 23, wherein detecting a similarity is accomplished by a pattern recognition method selected from the group consisting of statistical pattern recognition methods, artificial intelligence pattern recognition methods, and combinations thereof.

25. (Previously presented) The method of claim 20, wherein the derived relationship comprises proportional differences in individual elements of the fingerprint spectra of the second microorganism between the first and second sets of environmental factors.

26. (Previously presented) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain class of physiologically similar bacteria and the second, presumably metabolically similar microorganism belongs to the same class of physiologically similar bacteria, but the first and second microorganisms belong to different genera of bacteria of the same class of physiologically similar bacteria.

27. (Previously presented) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain genus of bacteria and the second, presumably metabolically similar microorganism is of the same genus of bacteria, but the first and second microorganisms belong to different species of bacteria of the same genus of bacteria.

28. (Previously presented) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain species of bacteria and the second, presumably metabolically similar microorganism is of the same species of bacteria, but the first and second microorganisms belong to different strains of the same species of bacteria.

29. (Previously presented) The method of claim 20, wherein the second, presumably metabolically similar microorganism is a representative of a metabolic similarity group that exhibits a fingerprint spectrum that is closest in canonical variate or principal component space to the fingerprint spectrum exhibited by the first microorganism under the first set of environmental conditions.

30. (Previously presented) The method of claim 29, wherein the second, presumably metabolically similar microorganism is a distance-weighted composite of two or more representatives of metabolic similarity groups.

31. (Previously presented) The method of claim 20, wherein the first set of environmental factors and the second set of environmental factors comprise the same batch of the same growth medium and the first set of environmental factors and the second set of environmental factors differ in at least one parameter selected from the group consisting of temperature, pressure, exposure to light, and exposure to gases.

32. (Previously presented) The method of claim 20, wherein the method is computer implemented.

Claims 33-66 (Canceled)

67. (Previously presented) The method of claim 20, wherein the first and second sets of environmental factors comprise different growth media.

68. (Previously presented) The method of claim 20, wherein the first and second sets of environmental factors comprise two batches of the same type of growth media.

69. (Previously presented) The method of claim 20, wherein the fingerprint spectra are pyrolysis mass spectra.

70. (Previously presented) The method of claim 20 further comprising adding the expected spectrum of the first microorganism to a database.

71. (Previously presented) The method of claim 31, wherein the first and second sets of environmental factors differ in temperature.

Claims 72-80 (Canceled).

[[--]]81. (Currently amended) A method for compensating for drift in fingerprint spectra due to differences in environmental factors that affect the metabolic state of microorganisms, wherein the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass spectra, MAB mass spectra, MALDI mass spectra, ESI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof, comprising:

culturing under a first set of environmental factors a first microorganism and a second microorganism that is presumably metabolically similar to the first microorganism;

measuring a fingerprint spectrum of the first microorganism cultured under the first set of environmental factors and a fingerprint spectrum of the second microorganism cultured under the first set of environmental factors;

obtaining a fingerprint spectrum of the second microorganism cultured under a second set of environmental factors that differ from the first set of environmental factors and affect the metabolic state of the first and second microorganisms;

deriving a relationship between the fingerprint spectrum of the second microorganism cultured under the first set of environmental factors and the fingerprint spectrum of the second microorganism cultured under the second set of environmental factors; and,

applying the relationship derived for the second microorganism to transform the fingerprint spectrum of the first microorganism cultured under the first set of environmental factors to an expected fingerprint spectrum for the first microorganism under the second set of

environmental factors that is compensated for drift due to the differences between the first and second sets of environmental factors that affect the metabolic state of the first microorganism.

82. (Cancelled)

83. (Previously presented) A method for compensating for drift in fingerprint spectra due to differences in environmental factors that affect the metabolic state of microorganisms, comprising:

culturing under a first set of environmental factors a first microorganism and a second microorganism that is presumably metabolically similar to the first microorganism;

measuring a pyrolysis mass spectrum of the first microorganism cultured under the first set of environmental factors and a pyrolysis mass spectrum of the second microorganism cultured under the first set of environmental factors;

obtaining a pyrolysis mass spectrum of the second microorganism cultured under a second set of environmental factors that differ from the first set of environmental factors and affect the metabolic state of the first and second microorganisms;

deriving a relationship between the pyrolysis mass spectrum of the second microorganism cultured under the first set of environmental factors and the pyrolysis mass spectrum of the second microorganism cultured under the second set of environmental factors; and,

applying the relationship derived for the second microorganism to transform the pyrolysis mass spectrum of the first microorganism cultured under the first set of environmental factors to an expected pyrolysis mass spectrum for the first microorganism under the second set of environmental factors that is compensated for drift due to the differences between the first and second sets of environmental factors that affect the metabolic state of the first microorganism.

84-88 (Canceled)

89. (Currently amended) The method of claim 20, wherein the mass spectra are electron impact, pyrolysis, MALDI, ~~CI,~~ ESI, nanospray, ~~APCI~~ or MAB mass spectra.

90. (Previously presented) The method of claim 20, wherein the infrared spectra are Fourier-transform infrared spectra, diffuse reflectance infrared spectra or attenuated total reflectance infrared spectra.

91. (Previously presented) The method of claim 20, wherein the gas chromatograms are chromatograms of derivatized cellular fatty acids, sugars, or amino acids.

92. (Previously presented) The method of claim 91, wherein the gas chromatograms are fatty-acid methyl ester gas chromatograms.

93. (Previously presented) The method of claim 20, wherein the liquid chromatograms are high-performance liquid chromatograms of proteins, nucleic acids, lipids or sugars.

94. (Currently amended) The method of claim 20, wherein the nuclear magnetic resonance spectra are ^{13}C, ^{1}H, ^{15}N, ^{19}F, ^{31}P, or two-dimensional homonuclear or heteronuclear magnetic resonance spectra. [[--]]